

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 8, 2002, 20:52:14 ; Search time 1153.49 Seconds  
(without alignments)  
12688.233 Million cell updates/sec

Title: US-09-635-521A-1

Perfect score: 1362  
Sequence: 1 atggcttaccacagctccc.....ttcagagacatgaatttga 1362

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Maximum Match 100%  
Listing first 45 summaries

Database: EST.\*

1: em\_estfun:\*  
2: em\_estlum:\*  
3: em\_estlin:\*  
4: em\_estom:\*  
5: em\_estpl:\*  
6: em\_estba:\*  
7: em\_estov:\*  
8: em\_estov:\*  
9: em\_hic:\*  
10: qb\_estl:\*  
11: qb\_est2:\*  
12: qb\_hic:\*  
13: qb\_gss:\*  
14: em\_gss\_fun:\*  
15: em\_gss\_hum:\*  
16: em\_gss\_inv:\*  
17: em\_gss\_pln:\*  
18: em\_gss\_pro:\*  
19: em\_gss\_rnd:\*  
20: em\_gss\_vit:\*  
21: em\_gss\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
C 1	508.6	37.3	676	10	BE385990 601276636
C 2	503.6	37.0	591	10	BE385990 601276636
C 3	502.4	36.9	534	10	BE385990 601276636
C 4	494.4	36.3	814	10	AL567376
C 5	479.8	35.2	578	10	AL567376
C 6	471.2	34.6	759	11	BE125134
C 7	464	34.1	843	11	BE125134
C 8	429.6	31.5	678	10	AL567376
C 9	413.6	30.4	460	10	AL567376
C 10	409.2	29.9	690	10	AW149665
C 11	406.6	29.9	821	11	BG752229
C 12	386	28.3	387	10	AT272281

13	383	28.1	649	10	AM590950
14	379.8	27.9	645	11	BE432379
15	371.2	27.3	699	10	BE395581
16	367.4	27.0	616	10	AI990500
17	361.6	26.5	696	11	BE439382
18	341.8	25.1	381	10	AA834860
19	336.6	24.7	396	10	AA613995
20	324.8	23.8	433	10	AA417651
21	305.6	22.4	551	11	BE858216
22	304.6	22.4	396	10	AI499630
23	303.6	22.3	558	10	AA173383
24	299.6	22.0	589	10	AI859538
25	294	21.6	540	11	BE939693
26	293	21.5	561	10	AM507899
27	292.6	21.5	537	11	BE594242
28	287.6	21.1	1130	12	AK016817
29	285	20.9	1490	12	AK012406
30	278.6	20.5	537	10	AI018769
31	274.6	20.2	549	10	AM652744
32	273.2	20.1	379	10	AI869176
33	268.6	19.7	527	10	AM338938
34	268.2	19.7	395	13	BH045199
35	265.6	19.5	515	10	AI336858
36	264.8	19.4	520	10	BE480975
37	251.4	18.5	367	10	AA780222
38	250.4	18.4	500	10	AM075598
39	249.4	18.3	640	10	AM148557
40	243	17.8	476	11	BF072978
41	240	17.6	368	11	BF935708
42	240	17.6	424	10	AM437808
43	238	17.5	379	10	AA084248
44	229.6	16.9	480	10	AI423162
45	228.6	16.8	313	10	AI480207

#### ALIGNMENTS

RESULT 1  
LOCUS BE385990/c 676 bp mRNA  
DEFINITION 601276636F1 NIH\_MGC.20 Homo sapiens CDNA clone IMAGE:361766 5',  
mRNA sequence.  
ACCESSION BE385990  
VERSION BE385990.1 GI:9331355  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE NIH-MGC http://mgi.ncl.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-r@mail.nih.gov  
Tissue Procurement: ATCC/DCPD/DP  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at: Image.llnl.gov  
Plate: LINC285 row: g column: 09  
High quality sequence stop: 653.

#### FEATURES

Location/Qualifiers  
1..676  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:361766"  
/clone\_lib="NIH\_MGC.20"  
/tissue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: skin; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
/note=""

ECORI: cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(c). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). "

Query Match	37.3%	Score 508.6;	DB 10;	Length 676;
Best Local Similarity	99.28;	Pred. No. 2e-101;		
Matches 511; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

QY	848	tcttcctcgaagcctbatagttctgtgcacatttgccgtatbctctgaatgcccacaacgaatttcgga	907
Db	530	TCtGCCAGGcCTaTtTGtTGtGACaTtGGcCGtATtGCTGGAItGGCCACACaATTTCGGA	471
QY	908	ggatcattgactgtcgcgccaaacccaagcagacttggacgaagttcctacttcggggtacaa	967
Db	470	GGATCAATGGCTGCGGCCAAACCCAAAGCACAGCTGGAGAGAGTCTCACTTCCGGGCTTACA	411
QY	968	tgaatccctccccccttcctcgagaagcttttctaccccaagctggtacatcaacccgctcc	1022
Db	410	TGAATCTCTCCCTTCTTCGGAGACGTTTTCtACTCACTGGTGTATCAACCCGCTCC	351
QY	1028	tgtacacggtgtccctcgcgaagcttcgcgagtglttcgtcaagttgtctgtcgcgc	108
Db	350	TGTACACAGGtGTCTCTCCACACAGTTTCGGGGGtGTTCGTGCAGGtGTCTGTGCTGCCGC	291
QY	1088	tgtctgcgcgcgcgcgcgaacccagcagaagaagcgcctgcgcgtacatgtgcactccacaacg	114
Db	290	TGTGTCTGCAGCAGCCACAGCCACACAGAGAGGCGCTGGCGCTACtTGGCGCACTCCACACCG	231
QY	1148	acagcgcgcgccttctgtgcagcgcccgcttgctcttcctgcggtccgcgcgcagctcctgcga	120
Db	230	ACACGCGCCCTTGTGTGCACAGCGCCGCTGTCTTCGCTCCGCGCCACAGTCTTCGCA	171
QY	1208	ggagaacttgaagaagatttcttaagcaactttcaagcgcgcgcgcgcgcgcgcgcgcgcgaat	126
Db	170	GGAGAACTGGAAAGATTTCCTTAAGCACTTTTCAGAGCGAGGCCGAGCCCAAGTCTAACT	111
QY	1268	cccaagtattgaatctcagatcactaagagcccaactcaagcgcgcgaacaacagccaattctcg	1327
Db	110	CCCAGTATTGAATCTCGAATCACTAGAGGCCCAACTCAGGCGGGAACACGCAATTCG	51
QY	1328	cttcagagaatagtcttcagaggaacatgaagtgtga	1362
Db	50	CTTGAGGAATGTCTTCAGACATGAAGTTTGA	16

RESULT	2
LOCUS	A1884686
DEFINITION	A1884686 591 bp mRNA EST 07-MAR-2000 W183d07.x1 NCI-CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2431501 3'
ACCESSION	GPR39. ; mRNA sequence.
VERSION	A1884686
KEYWORDS	A1884686.1 GI:5589850
SOURCE	EST.
ORGANISM	human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 591) NCI/NINDS-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> . National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTCAP), Tumor Gene Index unpublished (1998)
JOURNAL	Contact: Robert Strausberg, Ph.D.
COMMENT	Email: cgapbs-re@mail.nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Ronaldo, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution Information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bdrrp/image/image.html](http://www-bio.llnl.gov/bdrrp/image/image.html)  
Insert Length: 1462 Std Error: 0.00  
Seq Primer: -400P from GLBCO  
High quality sequence stop: 444.  
Location/Qualifiers  
1. 591

FEATURES	SOURCE
Location/Qualifiers	1..591
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="IMAGE:2431501"	
/clone_id="NCI_CGAP_Brn25"	
/tissue_type="anaplastic oligodendroglioma"	
/lab_host="DH108"	
/note="Organ: brain; Vector: pT7p3D-Pac (Pharmacia) with a modified polylinker; Site:1: Not I; Site2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'] TGTTACCAATCTGAAGTGGAGGCGCGCATGATTTTTTTTTTTTTTTT T 3']; Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7p3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."	
BASE COUNT	109 a 179 c 147 g 155 t 1 others
ORIGIN	

Query Match	Best Local Similarity	37.0%;	Score 503.6;	DB 10;	Length 591;
Matches	506;	Conservative	0;	Mismatches	5;
				Indels	0;
				Gaps	0;
QY	848	tcttccttgagcgtatattgtttgtgacatttggccgtatcgtatgacatgccaaacagttcga	907		
Db	80	TCCTCCAGGGCGTATGTTGTGACATTGGCCGATCGATCGATGCCAACAGATTCGGA	139		
QY	908	ggatcatgagctgcggcccaaacccaagaacagatctggaagaggttctactattccggcgtaca	967		
Db	140	GGATCATAGCGTCGCGCCAAACCCAGAGCAGCTGGAGAGAGTCTTACTTCGGGCGTACA	199		
QY	968	tgaatccctccccccttcctcgagaagcttttctaacctcagctcgatcatcaaccgcttc	1027		
Db	200	TGAATCTCTCTCCCTTTCTCGSAGACGTTTTTCTACTCTCACTCGGTATTAACCCGCTCC	259		
QY	1028	tgtaacagctgtcctcgcgaacagtttcgcgcggtgtgttcgtgcagtgctgtgtcgcgc	1087		
Db	260	TGTACACGGTGTCTCTCGACACAGTTTCGGCGGGGTTCTGTAAGAGTGTCTGTGCTGCC	319		
QY	1088	tgctgcctgcagcagccaaccaagagaagcgctgcgctacatgtgcactcaaccaacg	1147		
Db	320	TGTGCTGCGACGACGCCAACACAGAGAAGGCGCTCGCGCTGATATGCGCACTCCACACACG	379		
QY	1148	acagcgccgcttgtgcagcgccgctgtctcttcgcgctccgcagcgccagcttcctgcga	1207		
Db	380	ACAGCGCCCGCTTTGTGCACGCGCCGCTGTCTCTTCGCGTCCGGCGCCAGTCTCTGCAA	439		
QY	1208	ggaagaactgaaagatttcttaagcactttcagaagcgagcgccgaacccagttctaagt	1267		
Db	440	GGAGAACTGAGAAGATTTTCTTAAGCACTTTTCAGAGCGAGCGCCAGCCCACTTAAGT	499		
QY	1268	cccaagtcatttgatctctcgatctacatagagcccaactcgaagcgcgaaacagccaattctg	1327		
Db	500	CCAGTCATTGAATCTCGAGTCACTAAGGCCAATCTAGCGGAAACGACCAATTTCTG	559		
QY	1328	ctgcagagaatgttttcaggaagcatgaagt	1358		
Db	560	CTGCAGAGAAATGCTTTTCAGAGACATGAAGT	590		



QY 1028 tctacacggtgctccgcagcagcttctcgcgggtgtctgtcagtgctgtcgcgc 1087  
 |||||  
 Db 266 TGTACACGAGTGTCTCGACAGAGTTTGGGGGTTGTCGACAGTGTCTGTGCGCC 325  
 |||||  
 QY 1088 tctcgtcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1147  
 |||||  
 Db 326 TGTGTGTCGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 385  
 |||||  
 QY 1148 acagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1207  
 |||||  
 Db 386 ACAGCCGCCCTTTGTCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 445  
 |||||  
 QY 1208 ggaagacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1267  
 |||||  
 Db 446 GGAAGACTGAGAGATTTTAAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 505  
 |||||  
 QY 1268 cccagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag 1327  
 |||||  
 Db 506 CCCAGTATGAGTCTCGAGTATTTAGAGCCCACTCAGGGGNGAACAAGCCCAATTCTG 565  
 |||||  
 QY 1328 ctgcagagagtggttctcagagcagcagcagcagcagcagcagcagcagcagc 1362  
 |||||  
 Db 566 CTCGACAGAGATGCTTTTCAGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 600  
 |||||

RESULT 5  
 AIT742092 578 bp mRNA EST 19-DEC-1999  
 LOCUS AIT742092  
 DEFINITION W38H03.x1 Soares\_NSF\_P8\_9W\_OT\_PA\_P.S1 Homo sapiens cDNA clone  
 IMAGE:267413.3, similar to SW:GP99\_HUMAN O43194 PUTATIVE G  
 PROTEIN-COUPLED RECEPTOR GPR39, mRNA sequence.  
 AIT742092  
 VERSION AIT742092.1 GI:5110380  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 578)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP).  
 Tumor Gene Index  
 Unpublished (1997)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
 Insert Length: 806 Std Error: 0.00  
 Seq primer: 400P from Gibco  
 High quality sequence stop: 460.  
 Location/Qualifiers  
 1..578  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2367413"  
 /clone\_lib="Soares\_NSF\_P8\_9W\_OT\_PA\_P.S1"  
 /lab\_host="DH10B"  
 /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with  
 a modified polylinker; Site: 1: Not I; Site 2: Eco RI;  
 Equal amounts of plasmid DNA from five normalized  
 libraries were mixed, and ss circles were made in vitro.  
 Following HAP purification, this DNA was used as tracer in  
 a subtractive hybridization reaction. The driver was  
 PCR-amplified cDNAs from pools of 5,000 clones made from  
 the same 5 libraries. The pools consisted of the following  
 libraries and clones: Soares NBHSF pool 1:  
 309384-310919, 323208-325895 Soares NB2HF pool 1:  
 145032-147335, 147720-148103, 148872-149255, 15002 -  
 150407, 151176-152327 Soares NB2HF-9W pool 1:  
 758280-760583, 772104-774407 Soares NBHPA pool 1:  
 304776-306311, 320136-322823, 326280-326663 Soares NBHOT  
 pool 1: 723720-726407, 739080-740999 Subtraction by Bento

BASE COUNT 102 a 176 c 142 g 158 t  
 ORIGIN  
 Query Match 35.2%; Score 479.8; DB 10; Length 578;  
 Best Local Similarity 98.6%; Pred. No. 4e-95;  
 Matches 484; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 848 tcttcctgagtgatgtgtgtgacattggccgtatgctgatatcccaagattgga 907  
 |||||  
 Db 88 TCTGCCAAGGCTGATTGTTGACATTGGCGGTATGCTGATGCCCAACAGATTCGGA 147  
 |||||  
 QY 908 ggaatagctcgcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 967  
 |||||  
 Db 148 GATATATGCTCTGGCCCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 207  
 |||||  
 QY 968 tgatccctccctccctccctccctccctccctccctccctccctccctccctcc 1027  
 |||||  
 Db 208 TGATCCTCCTCCCTCTCTCGAGAGCTTTTCTACCTCAGCTCGGTATCAACCGTTCC 267  
 |||||  
 QY 1028 tctacacggtgctccgcagcagcagcagcagcagcagcagcagcagcagcagcagc 1087  
 |||||  
 Db 268 TGTACACGAGTGTCTCGACAGAGTTTGGGGGTTGTCGACAGTGTCTGTGCGCC 327  
 |||||  
 QY 1088 tctcgtcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1147  
 |||||  
 Db 328 TGTGCTCGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 387  
 |||||  
 QY 1148 acagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1207  
 |||||  
 Db 388 ACAGCGCCCGCTTGTGTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 447  
 |||||  
 QY 1208 ggaagacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1267  
 |||||  
 Db 448 GGAAGACTGAGAGATTTTAAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 507  
 |||||  
 QY 1268 cccagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag 1327  
 |||||  
 Db 508 CCCAGTATGAGTCTCGAGTATTTAGAGCCCACTCAGGGGNGAACAAGCCCAATTCTG 567  
 |||||  
 QY 1328 ctgcagagagat 1338  
 |||||  
 Db 568 CTCGACAGAGAT 578  
 |||||

RESULT 6  
 BF126050 759 bp mRNA EST 24-OCT-2000  
 LOCUS BF126050/c  
 DEFINITION 601762888F1 NIH\_MGC\_20 Homo sapiens cDNA clone IMAGE:4026092.5,  
 mRNA sequence.  
 BF126050  
 VERSION BF126050.1 GI:10965090  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 759)  
 NCI-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
 Tissue Procurement: ATCC/DCMB/DMP  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Inocyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at: [image.llnl.gov](mailto:image.llnl.gov)  
 Plate: LICM855 row: o column: 21  
 High quality sequence stop: 723.  
 Location/Qualifiers



RESULT	8								
LOCUS	A1936826								
DEFINITION	A1936826 678 bp mRNA EST 08-MAR-2000								
	w699h10.x1	NCI-CGAP-Brn25	Homo sapiens	CDNA	clone IMAGE:2467075	3'			
	similar to SW:G839.HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR								
	GPR39	;	mRNA sequence.						
ACCESSION	A1936826								
VERSION	A1936826.1	GI:5675696							
KEYWORDS	EST.								
SOURCE	human.								
ORGANISM	Homo sapiens								
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								
REFERENCE	1 (bases 1 to 678)								
AUTHORS	NCI/NIHDS-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .								
TITLE	National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/Brn25), Tumor Gene Index								
	Unpublished. (1998)								
CONTACT	Contact: Robert Strausberg, Ph.D.								

Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
[www.bio.ln1.gov/bdrp/image/image.html](http://www.bio.ln1.gov/bdrp/image/image.html)  
Insert length: 1143 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 454.  
Location/Qualifiers  
I. 678

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2467075"
/clone_1db="NCI-CGAP_Brn25"
/russue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/note="Organ: brain; Vector: pT7ad-Pac (Pharmacia) with a
modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTCACCAATCTGAAGTGGAGGCGCCGCAATGATTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

```

Query Match	31.5%;	Score 429, 6;	DB 10,	Length 678;
Best Local Similarity	98.4%;	Pred. 0, 1e-84;		
Matches 432;	Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0;
QY	848	tcttcctcgagcctgatagtgtgtgacatctgcccgtatctgtgatactccaacagattcgga	907	
Db	239	TCGTCCCAAGGGCTATTATTGTGTGTGACATTGGCCGTATGTGGATGGCCCAACAGATTCCGA	298	
QY	908	ggatcatgagctgcyggccaacccaagaacagactgtgacgaggttcttactctccgggcygtaca	967	
Db	299	GGATCATGCGCTCGGCCCAACCCCAAGCACAGCTGTGACAGCGTCTACTTCGGGGCGTACA	358	
QY	968	tgatcctcctccctcttcgcgagacgctttttctacactgaagtcggtacataaccgcgtcc	1027	
Db	359	TGATCCTCTCTCCCTTCTCGGAGACGTTTCTTACCTTACGTCGGTCTATCAACCGCGTCC	418	
QY	1028	tgtacaaggtgtctctcgacagcagtttcggcggggtgttcgtgcgaagtgtctgtctgcgcg	1087	

Db 419 TGTACAGGGTCTCCTCGCAGCAGTTTCGGCGGGGTGTTGTCGTCAGAGTGTGCGTGCAGCC 478

Oy 1088 tttctgctgcagcagcgcccaaccagagaaagcgctgcgctgcatcgatcgcatccaccacgg 1147

Db 479 TGTGCGTGCAGCAGCGCCACACGAGAAAGCGCTGCGGTACATGCGCAGCTCCACACG 558

Oy 1148 acagcgccgcctttgtgcagcgcccgcttgctcttcgcgtgccgcgagcgccagtcctctgcga 1207

Db 539 ACAAGCGCCGCTTTGTGACAGCGCGCGTTGCTTGTGCGTCCCGCGCCAGTCCGTGCGAN 598

Oy 1208 gggagactgtgaaagatcttcttaagcacttttcagagcgagcgcgagcccccagttctaagt 1267

Db 599 GGAAGATGTGAAGAAANNCTTAAACACTTTTCAGAGCGAGCGGACCCCACTTAAGT 658

Oy 1268 cccagtcattgattctcga 1286

Db 659 CCCAGTCATTGAGTCTCGA 677

RESULT	9
LOCUS	AI937602
DEFINITION	AI937602 460 bp mRNA
	WP81407.x1 NC_116267.1 Homo sapiens CDNA clone IMAGE:2468197 3'
	Similar to SW:GP39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
	GP39.1, mRNA sequence.
ACCESSION	AI937602
VERSION	AI937602.1
KEYWORDS	GI:5676472
SOURCE	EST.
ORGANISM	human.

ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE	1 (bases 1 to 460)
AUTHORS	NCBI/NIHNS-CCGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .
TITLE	National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CCGAP/BRGAP), Tumor Gene Index Unpublished (1998)
JOURNAL	
COMMENT	Contact: Robert Strausberg, Ph.D.

JOURNAL	COMMENT
Unpublished (1998)	
Contact: Robert Strausberg, Ph.D.	
Email: cgrabs-r@mail.nih.gov	
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.	
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.	
cDNA Library Arrayed by: Greg Lennon, Ph.D.	
DNA Sequencing by: Washington University Genome Sequencing Center	
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://www-bio.llnl.gov/dbip/lmage/lmage.html">www-bio.llnl.gov/dbip/lmage/lmage.html</a>	
Trace considered overall poor quality	
Insert Length: 689 Std Error: 0.00	
Seq Primer: -40UP from Glibco	
High quality sequence stop: 1.	
Location/Qualifiers	
1. .460	

```

FEATURES
source
Location/Qualifiers
1..460
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cdate="IMAGE:2468197"
/clone_11b="NCL CGAP-Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pT773D-Pac (Pharmacia) with a
modified polylinker. Site.1: Not I; Site.2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTCACATCTGAGTGGAGGCGGCCGACATGGTTTATTTTATTTTATTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT773 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT
95 a 155 c 115 g 95 t

```









Db	207	TCGAGCAGTTTCGGGCGGGTGTGTGGAGGTGCTGTCTGCGCTTCGCTGGAGCAC	148
Qy	1102	gccaaccaaggaagcgccctgcggtacatcgcacccaacccaagcgccgcttt	1161
Db	147	GCCAAACCGAGAAAGCCGCTGCGGTACATGCGCACTCCACACGAGCGCCGCTTT	88
Qy	1162	gttagagcgccgctgtccttcctgcgtcccgcgcgccaagtcctctcgaaggaagacttgaag	1221
Db	87	GTCGAGCCCGCTGTCCTTTGGCTCCCGCGGCCAGTCTCTGCAGAAGAACTGAGAG	28
Qy	1222	attctcctaagcacttttcagaagcgag	1248
Db	27	ATTTCCTTAAGCACTTTTCAGAGCGAG	1

RESULT	13
LOCUS	AM590950
DEFINITION	AM590950 649 bp mRNA EST 22-MAR-2000
ACCESSION	U51212.x1 NC1_CGAG-GC6 Homo sapiens cDNA clone IMAGE:2949166 3'
VERSION	similar to SW:GP39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
KEYWORDS	GP39, ; mRNA sequence.
SOURCE	AM590950
	AM590950.1 GI:7278094
	EST.
	human.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 649)  
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph. D.

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/INTL at: [Image.llnl.gov/image/html/resources.shtml](http://Image.llnl.gov/image/html/resources.shtml)

Possible reversed clone: similarity on wrong strand  
Seq primer: -40UP from Glbco  
High quality sequence stop: 457.

Location/Qualifiers  
1. 649  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="294916"  
/clone\_id="NCI CGAP GC6"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/note="Vector: pT7MD-Pac (Pharmacia) with a modified polylinker. Site 1: Not I. Site 2: Eco RI. Plasmid DNA from the normalized library NCI-CGAP-GC4 was prepared, and 58 clones were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

Query Match	28.1%;	Score 383;	DB 10;	Length 649;
Best Local Similarity	97.3%;	Pred. No. 6.6e-74;		
Matches 400; Conservative	0;	Mismatches 10;	Indels 1;	Gaps 1

[illegible]

RESULT	14
BF432379	
LOCUS	645 bp mRNA
DEFINITION	mac59i11.x1 NC1.CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3406292 3'
	similar to SW:GP39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
ACCESSION	GP39. ; mRNA sequence.
VERSION	BF432379
KEYWORDS	BF432379.1 GI:11444509
SOURCE	EST.
	human.

REFERENCE AUTHORS TITLE	JOURNAL COMMENT
Makayofa; Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi; Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo. 1 (Phase 1 to 645)	
NCI/NIHNS-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> . National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BrGAP), Tumor Gene Index Unpublished (1998)	
Contact: Robert Strausberg Ph.D.	

Ph.D.  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL, send email to:  
info@image.llnl.gov  
Seg primer: -40UP from Gibco  
High quality sequence stop: 441.  
Location/Qualifiers  
1. .645  
source

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3406292"
/clone_1b="NCLCGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pTRT3D-Pac (Pharmacia) with a
modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTCACATCTGAAGTGGAGGCGCCGATACCTTTTTTTTTTTTTTTTTTTT

```



Wed Jan 9 08:51:39 2002

us-09-635-521a-1.rst

---

Page 11

